HIV vaccine-research team shifts to SARS-CoV-2

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Building on previous work designing an experimental HIV vaccine being tested in two human vaccine efficacy trials, the Los Alamos National Laboratory HIV team is now deploying its expertise in genetic databases and bioinformatics against the novel coronavirus SARS-CoV-2, the virus that causes the COVID-19 disease.

Three main thrusts are underway from the HIV team: developing a T-cell response vaccine approach, tracking the origin of the pathogen, and building a robust bioinformatics pipeline to track the virus's evolution. While this work focuses on attacking the virus itself, other bioinformatics and modeling efforts across the Laboratory aim at predicting disease spread to support decision making by government and health agencies.

Developing a T-cell response vaccine approach

Bette Korber, a computational biologist and the driving force behind the "mosaic" vaccine concept for HIV, together with fellow scientists Will Fischer and Sandrasegaram Gnanakaran, is shifting her attention from HIV, ebola, and influenza vaccines to developing a T-cell based vaccine design for the SARS CoV-2 coronavirus.

Traditional antibody vaccines are primarily intended to reduce rates of infection. Korber says they hope that vaccine-elicited T-cell responses could help ameliorate disease severity if people do get infected, and so this approach could be used to complement antibody-based vaccines. Korber and the HIV team members are in the Laboratory's Theoretical Biology and Biophysics group.

Tracking the origin of the pathogen

Elena Giorgi, also of the Theoretical Biology and Biophysics group, recently published a pre-print paper on the origins of the virus,"Emergence of SARS-CoV-2 through Recombination and Strong Purifying Selection."

"Our team demonstrated, by looking at the genetic sequence of the virus and comparing it to other known coronaviruses, that it originated from animals," said Giorgi. "More specifically, it most likely came from a family of bat viruses that acquired the ability to infect human cells from another family of coronaviruses found in pangolins."

Developing a robust bioinformatics pipeline

The Laboratory's HIV database team led by Korber is now developing a real-time bioinformatics pipeline to track the evolution of the SARS Cov-2 spike protein, the target of the antibody-based vaccine approaches that are currently under development by many different groups worldwide. The implementation of this pipeline is being led by Will Fischer, Hyejin Yoon, and Werner Abfalterer.

The team is working to ensure that the evolving SARS Cov-2 variants that will be circulating when the vaccine is ready for delivery will remain sensitive to vaccine responses elicited using a spike protein based on the original strain that seeded the pandemic. As part of this effort, Gnanakaran will be modeling the molecular dynamics of the SARS Cov-2 spike protein and the sugars on its surface, to better understand the impact of the mutations that are beginning to accumulate in the circulating population.

They will also be adapting vaccine strategies they developed for HIV, which is a very diverse virus, to attempt to design vaccines that could work not only against the current pandemic virus, which is quite conserved, but also against highly diverse reservoir of coronaviruses that circulate in bats and other animals.

"One of the risks that we've recognized with this coronavirus is that there is an immense pool of other coronaviruses hiding in bats and pangolins and snakes and whatnot. We would like to come up with a strategy to protect us, not just against this particular strain, but maybe next year's jump, too," said Nick Hengartner, leader of the Theoretical Biology and Biophysics group.

There is a regularly-updated news page on the Laboratory site with the latest information and media coverage of the Lab's scientific response to the emergency.